

Expression Console™ Software 1.1.1 Release Notes

The following issues from the Expression Console software version 1.1 have been addressed.

- In Expression Console 1.1 when a report or the probe set results table was sorted the row identifiers were not sorted. This only affected the display in the application, exporting the data had the correct assignment of row identifiers to the data columns even after sorting. This issue is fixed in 1.1.1, so that the entire table, including the row identifiers is now sorted in the displayed tables and reports.
- The NetAffx link in the Probe Level Summarization Report now works for Gene Arrays and for the Exon Arrays at both the Exon and Gene level. Double clicking on the probe id in the Probe Level Summarization Report now returns the results from the NetAffx query for that probe id.
- For Gene Arrays and Gene level analysis on Exon Array the mean of the background probes on the array (bgrd mean) is now reported instead of the mm mean when a background probe file (bgp file) is identified in the analysis configuration. This provides a better measure of the background signal on the array as there are few or no MM probes on the Gene and Exon Arrays.

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New Features and Enhancements

- The Expression Console 1.1 Software release provides support for the GeneChip® Human Gene 1.0 ST Array, which is the latest product in the family of Affymetrix expression arrays offering whole-transcript coverage.
 - Same simple analysis workflow using RMA to generate Probe Set signal estimates as 3' Expression and Exon Arrays.
 - Same visualization tools are used to examine the algorithm metrics and GeneChip data quality as for 3' Expression and Exon Arrays.
- A probe level summarization file can be generated by combining annotation information contained in comma-separated files (CSV files) with the signal values into a single tab-delimited file.
 - Expression Console downloads the Annotation CSV files directly from NetAffx.
 - Users can select the annotation information they want added to their results file (*e.g.*, Gene Symbol)
 - User created CSV files are supported
- Graphs and tables can be printed directly
- A Cancel button has been added to stop analyses.
- All the MvA plots can be drawn either with a dynamically selected scale for each graph, or a fixed scale defined by the user.

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The following issues from Expression Console software version 1.0 have been addressed.

- For Exon Arrays the ability to threshold a metric by comparing it to the average of that metric across all of the selected arrays by number of standard deviations has been fixed.
- For Exon Level analyses using DABG the report table now contains the AUC value for both the DABG and the PLIER algorithms.
- The first column of the probe set summarization table when exported as TXT is now labeled probe id.
- Exporting probe set summarization results as TXT files from multiple groups now places each group in its own file.

The following are the known issues that exist in the Expression Console™ Software version 1.1:

1. Group Names Missing in the Study window: Group names are not created in the Study window separating the CHP files from different analysis runs on Win 2K SP4.
2. Cannot Edit Metric in Report Thresholds before CHP File is created: The user cannot change the Metrics in the Report Thresholds dialog without having a study open that contains at least one CHP file. The workaround is to add at least one CHP file to the study and then modify the report thresholds.
3. NetAffx link in the Probe Level Summarization Report does not work for Exon data.
When a user views the Probe Level Summarization Report for an Exon array CHP file then double clicks on the probe id results, the results from NetAffx will state that the query returned no results.
The workaround is to click the probe sets query in the window that popped up and manually enter the probe id in the query window.
4. ZIP utility does not always include library files for Exon arrays.
The ZIP utility includes library files for Exon arrays only when CHP files are analyzed as part of the study. If the user creates a study and adds existing CHP files then the library files will not be included in the ZIP archive.
The workaround is to manually add the appropriate library files to the ZIP file. The library files can be found in the file properties for the CHP file.
5. Some memory intensive operations in the Expression Console software may run out of memory and provide an error message: Expression analysis especially on Exon Arrays can generate large amounts of data. It is possible that while using Expression Console the application

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will run out of memory and provide an error message. **Occasionally** multiple error messages will be generated if there is not enough memory to complete a series of requested actions. For example, attempting to simultaneously open several 10's of CEL files (actually number will depend on the amount of RAM currently available to the Expression Console software) in the intensity viewer may cause the application to run out of memory. An error message will be displayed for each CEL file that was not able to be displayed. Closing other applications or requesting fewer items to be simultaneously displayed will minimize this issue.

6. Not all of the functions within the Expression Console software have Progress Meters:
Exon arrays contain over 6 million probes organized into 1.4 million probe sets at the Exon level. Operations like Feature intensity box plots, and feature intensity views may take an extended amount of time to complete and they currently do not have progress meters. This will be addressed in a future release of Expression Console.
7. Renaming configuration files from the operating system causes errors:
Custom analysis configuration files are stored in the library file directory. Editing the name of the files outside of the application may cause the software to generate an error message when opening the configuration. The workaround for this issue is to open the configuration within Expression Console and select "Save As" and give the configuration a new name.
8. Probe sets may have a signal value equal to 0:
Probe sets that fail to analyze with the PLIER and RMA workflows have their signal values reported as "0". For example, performing an Exon Analysis on all of the probe sets on the Exon array results in failed analyses for the background probes, thus they have a reported signal value=0. This will be addressed in a future release of Expression Console.
9. In the MvA Plot, the Y-Axis of the graph will not display the negative sign when the value is 10 or greater.
10. All library files must be in the active library file folder to be recognized by the Expression Console Software. For example, on the Advanced Exon/Gene configuration page entering the full path to a file will produce an error stating that the file is not found. The workaround is to place all of the library files for a particular analysis configuration in a single folder and identify that as the current library file folder in the Expression Console software.
11. No graph is displayed if CHP file names are more than 115 characters:

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The workaround is to either enlarge the graph or user shorter CHP file names.